

GenCore version 4.5
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CM protein - protein search, using sw model

Run on: May 15, 2002, 07:57:59 ; Search time 33.64 seconds
(without alignments)
1397,311 Million cell updates/sec

Title: US-09-783-320-4

Reflected score: 6243
Sequence: 1 NEXYVRKRGKSGSFGKAIL.....YAKIHLMVMDAGVNDND 1214

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 105324 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105324

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 08
Maximum Match 1008
Listing first 45 summaries

Database: SwissProt_40.*

Prod. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Match	Length	DB ID	Description
1	3385	54.2	774	1	NEK1_MOUSE
2	847.5	13.6	841	1	STR2_HUMAN
3	833	13.3	511	1	NEK3_MOUSE
4	790.5	12.7	439	1	NEK4_HUMAN
5	763.5	9.1	431	1	NEK4_MOUSE
6	543.5	8.9	443	1	NEK2_MOUSE
7	530.5	8.5	459	1	NIMA_MOUSE
8	528.5	8.5	431	1	NIMA_MOUSE
9	502.5	8.0	1142	1	GIN4_YEAST
10	499.5	8.0	779	1	NIMA_MOUSE
11	468.5	7.5	966	1	STIO_MOUSE
12	455	7.3	968	1	STIO_MOUSE
13	455	7.3	1518	1	KKK1_HUMAN
14	437.5	7.0	915	1	KCC4_YEAST
15	432	6.9	435	1	KIN3_YEAST
16	421.5	6.8	1895	1	KIN3_MOUSE
17	393	6.3	1080	1	YKK1_MOUSE
18	388	6.2	1062	1	CCY_MOUSE
19	383.5	6.1	705	1	CCY_MOUSE
20	382.5	6.1	740	1	KKK1_HUMAN
21	382	6.1	740	1	KKK1_HUMAN
22	382	6.1	740	1	KKK1_HUMAN
23	380.5	6.1	682	1	SNK_MOUSE
24	380	6.1	682	1	SNK_MOUSE
25	379	6.1	682	1	SNK_MOUSE
26	378	6.1	682	1	SNK_MOUSE
27	378	6.1	682	1	SNK_MOUSE
28	378	6.1	682	1	SNK_MOUSE
29	378	6.1	682	1	SNK_MOUSE
30	378	6.1	682	1	SNK_MOUSE
31	378	6.1	682	1	SNK_MOUSE
32	377.5	6.0	733	1	KKK1_HUMAN
33	375	6.0	1305	1	GAR_MOUSE

ALIGNMENTS

RESULT ID	NEK1_MOUSE	STANDARD	PRT	774 AA
AC	01-0CT-1996 (Rel. 34, Created)			
DT	01-0CT-1996 (Rel. 34, Last sequence update)			
DT	16-0CT-2001 (Rel. 40, Last annotation update)			
DE	Serine/threonine-protein kinase NEK1 (EC 2.7.1.1) (NIMA-related protein kinase 1).			
GN	NEK1			
OS	NIMA-related (Mouse).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.			
OX	NCBI_TaxID:10090;			
RP	SEQUENCE FROM N.A.			
RC	TISSUE=Blood;			
RX	MEDLINE=33010942; PubMed=1382974;			
RA	Levin K., Mizzen L., Motro B., Ben-David Y., Bernstein A., Dawson T.;			
RT	"A mammalian dual specificity protein kinase, NEK1, is related to the NIMA cell cycle regulator and highly expressed in meiotic germ cells."			
RT	EMBO J. 11:3521-3531(1992).			
CC	- FUNCTION: PHOSPHORYLATES SERINES AND THREONINES, BUT ALSO APPEARS TO PHOSPHORYLATE TYROSINE KINASE ACTIVITY. IMPLICATED IN THE CONTROL OF MEIOSIS.			
CC	- SUBCELLULAR LOCATION: Nuclear (Probable).			
CC	- TISSUE SPECIFICITY: PREDOMINANTLY IN TESTES (CPM CELLS AND SPERMATOCYTES), LOWER LEVELS IN OVARY (OVOCYTES AND GRANULOSA CELLS), THYMUS, AND LUNG.			
CC	- DEVELOPMENTAL STAGE: IN FEMALE, EXPRESSED AS FOLLICLES ENTER THE SECONDARY STAGE UNTIL OVULATION OCCURS. IN THE MALE REPRODUCTIVE SYSTEM, THE EXPRESSION IS LIMITED TO SPERMATOCYTES AND SPERMATIDS.			
CC	- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.			
CC	- NIMA SUBFAMILY.			
CC	THIS SWISS-PROT ENTRY IS COPYRIGHTED. IT IS PRODUCED THROUGH A COLLABORATION BETWEEN THE SWISS INSTITUTE OF BIOINFORMATICS AND THE EMBL OUTSTATION - THE EUROPEAN BIOINFORMATICS INSTITUTE. THERE ARE NO RESTRICTIONS ON ITS USE BY NON-PROFIT INSTITUTIONS AS LONG AS ITS CONTENT IS IN NO WAY MODIFIED AND THIS STATEMENT IS NOT REMOVED. USAGE BY AND FOR COMMERCIAL ENTITIES REQUIRES A LICENSE AGREEMENT (SEE http://www.isb-sib.ch/announce/ or send an email to license@sib-sib.ch).			
CC	OR send an email to license@sib-sib.ch .			
CC	EMBL: S45828; AA023529.1;			
CC	HSP: P24841; JEM1.			
CC	MGI: M619703; Nek1.			
CC	InterPro: IPR000719; Ser_Thr_Kinase.			
CC	InterPro: IPR002290; Ser_Thr_Kinase.			
CC	Pfam: PF00069; Kinase; 1.			
CC	SMART: SM00220; S_TKc; 1.			
CC	PROSITE: PS00107; PROTEIN_KINASE_ATP; 1.			
CC	PROSITE: PS00108; PROTEIN_KINASE_ST; 1.			
CC	PROSITE: PS00011; PROTEIN_KINASE_DOM; 1.			
CC	Transferase: Serine/threonine-protein kinase; ATP-binding; Mitosis;			

34	374.5	6.0	982	1	SOLD_MOUSE
35	374	6.0	350	1	KAPC_HUMAN
36	374	6.0	615	1	CKR_MOUSE
37	374	6.0	745	1	KAPC_HUMAN
38	373.5	6.0	490	1	SPS1_YEAST
39	372	6.0	646	1	CKR_MOUSE
40	371.5	6.0	485	1	KAPC_MOUSE
41	371	5.9	371	1	KAPC_MOUSE
42	371	5.9	370	1	KAPC_MOUSE
43	371	5.9	370	1	KAPC_MOUSE
44	371	5.9	444	1	KAPC_MOUSE
45	369.5	5.9	397	1	KAPC_MOUSE

P46549	Caenorhabditis
P22612	homo sapiens
Q9R011	rattus norvegicus
Q9UK32	homo sapiens
P08458	saccharomyces
Q94344	homo sapiens
Q92144	mus musculus
P00217	bos taurus
P00217	homo sapiens
Q15112	homo sapiens
P51644	dictyostelium
P06244	saccharomyces

Nuclear protein: Phosphorylation: Cell cycle: Cell division:
 KW Tyrosine protein kinase
 FT DOMAIN 4 258 PROTEIN KINASE
 NP_BIND 10 18 ATP (BY SIMILARITY)
 BINDING 33 33 ATP (BY SIMILARITY)
 FT ACT_SITE 128 128 BY SIMILARITY
 SEQUENCE 774 AA; 88427 MW; 7E5E881ACD06FA CRC64;

Query Match 54.2%; Score 3385; DB 1; Length 774;
 Best Local Similarity 85.5%; Pred. No. 1,2e-118;
 Matches 665; Conservative 45; Mismatches 64; Indels 4; Gaps 3;

1 MEKYLRLKIGSGSPFKALVSTEDPROVYIKKINISMSKRESESRREAVLANMKH 60
 1 MEKYLRLKIGSGSPFKALVSTEDPROVYIKKINISMSKRESESRREAVLANMKH 60
 61 PNIVYRESFEENGSLYIVMDYCEGDLFRINAGGVLFQEDQILDFQICLAKH 120
 61 PNIVYRESFEENGSLYIVMDYCEGDLFRINAGGVLFQEDQILDFQICLAKH 120
 61 PNIVYRESFEENGSLYIVMDYCEGDLFRINAGGVLFQEDQILDFQICLAKH 120
 121 DRKILHDIRSONIFLTKDGTQVLDGFIARVNSTVELARFCIGTPYISPEICENKPY 180
 121 DRKILHDIRSONIFLTKDGTQVLDGFIARVNSTVELARFCIGTPYISPEICENKPY 180
 121 DRKILHDIRSONIFLTKDGTQVLDGFIARVNSTVELARFCIGTPYISPEICENKPY 180
 181 NNSGDVNLGCVYELCTLKHAFENGSMKNLYLKITSGSPVSLHYSDLSVLSOLF 240
 181 NNSGDVNLGCVYELCTLKHAFENGSMKNLYLKITSGSPVSLHYSDLSVLSOLF 240
 181 NNSGDVNLGCVYELCTLKHAFENGSMKNLYLKITSGSPVSLHYSDLSVLSOLF 240
 241 RNPDRPSVNSITLKKFINKRIKFLPOLAEFECLKTSKSGSPVSPHYSDLSVLSOLF 240
 241 RNPDRPSVNSITLKKFINKRIKFLPOLAEFECLKTSKSGSPVSPHYSDLSVLSOLF 240
 241 RNPDRPSVNSITLKKFINKRIKFLPOLAEFECLKTSKSGSPVSPHYSDLSVLSOLF 240
 301 SYMPAKRTKTPANKYGIPLAYKRGDKRLHKKRPLQKHKQAKOHPKRNANGSEERKISE 360
 301 SYMPAKRTKTPANKYGIPLAYKRGDKRLHKKRPLQKHKQAKOHPKRNANGSEERKISE 360
 301 SYMPAKRTKTPANKYGIPLAYKRGDKRLHKKRPLQKHKQAKOHPKRNANGSEERKISE 360
 361 EAKRRRLFEFEKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 420
 361 EAKRRRLFEFEKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 420
 361 EAKRRRLFEFEKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKKK 420
 421 VAPPLSGGCTIAPSSFSRSGQYEHYHIFOMQOQAEDEKAKMRETYGGLPEKQK 480
 421 VAPPLSGGCTIAPSSFSRSGQYEHYHIFOMQOQAEDEKAKMRETYGGLPEKQK 480
 421 VAPPLSGGCTIAPSSFSRSGQYEHYHIFOMQOQAEDEKAKMRETYGGLPEKQK 480
 481 QLAVERAKOVVEFLQRRREAMONKARAGHVVYLAIRLOIRLQNFEROQIATKRGSK 540
 481 QLAVERAKOVVEFLQRRREAMONKARAGHVVYLAIRLOIRLQNFEROQIATKRGSK 540
 481 QLAVERAKOVVEFLQRRREAMONKARAGHVVYLAIRLOIRLQNFEROQIATKRGSK 540
 541 EAHNSEGGEGSEADNRKRIESTLKAHANNAVAALKEQLERKREKAYEREKKVMEHVA 600
 541 EAHNSEGGEGSEADNRKRIESTLKAHANNAVAALKEQLERKREKAYEREKKVMEHVA 600
 541 EAHNSEGGEGSEADNRKRIESTLKAHANNAVAALKEQLERKREKAYEREKKVMEHVA 600
 601 KGVKSSDVSPPLGQHEGSGSPKQOQMSVISTALKVEVDLSLDTRETSEEMOKTN 660
 601 KGVKSSDVSPPLGQHEGSGSPKQOQMSVISTALKVEVDLSLDTRETSEEMOKTN 660
 601 KGVKSSDVSPPLGQHEGSGSPKQOQMSVISTALKVEVDLSLDTRETSEEMOKTN 660
 661 AATSRREITRLNENLKAODEKQMONLSTFEINVEDAKKEHEKKSVSDRKMEAGC 720
 661 AATSRREITRLNENLKAODEKQMONLSTFEINVEDAKKEHEKKSVSDRKMEAGC 720
 661 AATSRREITRLNENLKAODEKQMONLSTFEINVEDAKKEHEKKSVSDRKMEAGC 720
 721 QLVIPDLDELDTSTSTTERHTVGEVYIKLPGSPRRAMKSPSTDVLLDEALQ 778
 721 QLVIPDLDELDTSTSTTERHTVGEVYIKLPGSPRRAMKSPSTDVLLDEALQ 778
 721 QLVIPDLDELDTSTSTTERHTVGEVYIKLPGSPRRAMKSPSTDVLLDEALQ 778

Serine/threonine protein kinase 2 (EC 2.7.1.37) (Serine/threonine-
 DE protein kinase NRK2).
 GN STRK2.
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
 OX NCBI_Taxid=9606;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE-BREAST;
 RX MEDLINE-94268838; PubMed-8208544;
 RA Levedakou E.N., He M., Baptist E.W., Craven R.J., Cance W.G.,
 RA Welch P.L., Simons A., Naylor S.L., Leach R.J., Lewis T.B.,
 RA Bowcock A., Liu E.T.;
 RA "Two novel human serine/threonine kinases with homologies to the cell
 cycle regulating Xenopus M015, and NIMA kinases: cloning and
 characterization of their expression pattern.";
 RT Oncogene 9:1977-1988(1994).
 CC -1- CATALYTIC ACTIVITY: ATP + a protein - ADP + a phosphoprotein.
 CC -1- SUBCELLULAR LOCATION: Nuclear (Probable).
 CC -1- TISSUE SPECIFICITY: HIGHEST EXPRESSION IN ADULT HEART, FOLLOWED BY
 CC PANCREAS, SKELETAL MUSCLE, BRAIN, LIVER, KIDNEY, LUNG AND
 CC PLACENTA. PRESENT IN MOST PRIMARY CARCINOMAS.
 CC -1- SIMILARITY: BELONGS TO THE SER/THR FAMILY OF PROTEIN KINASES.
 CC NIMA SUBFAMILY.
 CC
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 CC
 CC EMBL: L20321; AAA3658.1;
 CC HSSP: P11362; IFGK.
 CC
 CC DR MIM: 601959;
 CC DR InterPro: IPR000719; Euk_Pkinase.
 CC DR InterPro: IPR002290; Ser_thr_Pkinase.
 CC DR Pfam: PF00069; Pkinase.1.
 CC DR SMART: SM00220; S_TKC.1.
 CC DR PROSITE: PS00107; PROTEIN_KINASE_ATP.1.
 CC DR PROSITE: PS00108; PROTEIN_KINASE_ST.1.
 CC DR PROSITE: PS00111; PROTEIN_KINASE_DOM.1.
 CC KW Transferrase; Serine/threonine-protein kinase; ATP-binding; Mitosis;
 CC Nuclear protein; Phosphorylation.
 FT DOMAIN 261
 FT NP_BIND 12 20
 FT BINDING 35 35
 FT ACT_SITE 131 131
 FT MOD_RES 165 165
 FT SEQUENCE 841 AA; 94571 MW; 0DD31920DDE7E458 CRC64;
 SQ
 Query Match 13.6%; Score 847.5; DB 1; Length 841;
 Best Local Similarity 28.1%; Pred. No. 5,9e-75;
 Matches 263; Conservative 160; Mismatches 316; Indels 197; Gaps 34;

RESULT 2
 STRK2_HUMAN STANDARD; PRT; 841 AA.
 AC P51957;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)

123 KILHDIRSONIFLTKDGTQVLDGFIARVNSTVELARTCTGTPYISPEICENKPY 182
 126 HILHDIRSONIFLTKDGTQVLDGFIARVNSTVELARTCTGTPYISPEICENKPY 185
 183 KSDINALGCVYELCTLKHAFENGSMKNLYLKITSGSPVSLHYSDLSVLSOLF 242
 186 KSDVNLGCVYELCTLKHAFENGSMKNLYLKITSGSPVSLHYSDLSVLSOLF 245